

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:53:29 ; Search time 118.5 Seconds

(without alignments)
225.008 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gttctgctcgttc 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1/COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5/COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A/COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B/COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/H/COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PCTUS/COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/PP/COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/RE/COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	3	US-09-335-629-2
2	15	100.0	113	3	US-08-956-171E-4822
3	15	100.0	113	3	US-08-781-986A-4822
4	15	100.0	305	3	US-08-956-171E-4375
5	15	100.0	305	3	US-08-781-986A-4375
6	15	100.0	356	3	US-08-956-171E-4293
7	15	100.0	356	3	US-08-781-986A-4293
8	15	100.0	400	3	US-08-956-171E-3550
9	15	100.0	400	3	US-08-781-986A-3550
10	15	100.0	400	3	US-08-956-171E-3633
11	15	100.0	400	3	US-08-781-986A-3633
12	15	100.0	400	3	US-08-956-171E-3802
13	15	100.0	400	3	US-08-781-986A-3802
14	15	100.0	400	3	US-08-956-171E-4162
15	15	100.0	400	3	US-08-781-986A-4162
16	15	100.0	400	3	US-08-956-171E-1635
17	15	100.0	400	3	US-08-781-986A-1635
18	15	100.0	400	3	US-08-956-171E-1630
19	15	100.0	400	3	US-08-781-986A-1630
20	15	100.0	579	3	US-08-956-171E-1635
21	15	100.0	579	3	US-08-781-986A-1635
22	15	100.0	589	3	US-08-956-171E-3630
23	15	100.0	589	3	US-08-781-986A-3630
24	15	100.0	1171	3	US-08-956-171E-3539

Sequence 3539, Ap	US-08-781-986A-3539	1171	3	100.0	15	C 25
Sequence 3194, Ap	US-08-956-171E-3194	1290	3	100.0	15	C 26
Sequence 3194, Ap	US-08-781-986A-3194	1290	3	100.0	15	C 27
Sequence 6, Appli	US-09-726-774-6	1484	3	100.0	15	C 28
Sequence 160, App	US-08-757-653-160	1555	2	100.0	15	C 29
Sequence 160, App	US-08-520-946-160	1555	3	100.0	15	C 30
Sequence 160, App	US-09-653-378A-160	1555	3	100.0	15	C 31
Sequence 3552, Ap	US-08-956-171E-3552	2209	3	100.0	15	C 32
Sequence 3552, Ap	US-08-781-986A-3552	2209	3	100.0	15	C 33
Sequence 56, Appli	US-08-956-171E-56	30246	3	100.0	15	C 34
Sequence 56, Appli	US-08-781-986A-56	30246	3	100.0	15	C 35
Sequence 4790, Ap	US-08-956-171E-4790	89.3	129	89.3	13.4	C 36
Sequence 4790, Ap	US-08-781-986A-4790	89.3	129	89.3	13.4	C 37
Sequence 8865, Ap	US-09-902-540-8865	609	3	89.3	13.4	C 38
Sequence 902, App	US-09-270-767-902	611	3	89.3	13.4	C 39
Sequence 16184, A	US-09-270-767-16184	611	3	89.3	13.4	C 40
Sequence 1, Appli	US-09-503-505A-1	1362	3	89.3	13.4	C 41
Sequence 14070, A	US-09-270-767-14070	1697	3	89.3	13.4	C 42
Sequence 9, Appli	US-08-693-103B-9	2556	3	89.3	13.4	C 43
Sequence 9, Appli	US-09-229-059-9	2556	3	89.3	13.4	C 44
Sequence 9, Appli	US-08-628-133-9	2556	3	89.3	13.4	C 45
Sequence 11, Appli	US-08-699-103B-11	2731	3	89.3	13.4	C 46
Sequence 11, Appli	US-09-229-059-11	2731	3	89.3	13.4	C 47
Sequence 11, Appli	US-09-628-133-11	2731	3	89.3	13.4	C 48
Sequence 9, Appli	US-08-747-562-9	2866	3	89.3	13.4	C 49
Sequence 2, Appli	US-09-503-505A-2	3497	3	89.3	13.4	C 50
Sequence 5817, Ap	US-09-949-016-5817	3492	3	89.3	13.4	C 51
Sequence 944, App	US-09-949-016-944	8540	3	89.3	13.4	C 52
Sequence 17556, A	US-09-949-016-17556	74644	3	89.3	13.4	C 53
Sequence 13973, A	US-09-270-767-13973	1121	3	86.7	13	C 54
Sequence 10, Appli	US-09-725-957-10	1319	3	86.7	13	C 55
Sequence 13, Appli	US-09-725-957-13	1344	3	86.7	13	C 56
Sequence 1242, Ap	US-09-902-540-1242	28783	3	86.7	13	C 57
Sequence 287, App	US-08-952-793-287	97	3	82.7	12.4	C 58
Sequence 287, App	US-09-849-928-287	97	3	82.7	12.4	C 59
Sequence 287, App	PCT-US96-09455A-287	97	6	82.7	12.4	C 60
Sequence 40, Appli	US-08-181-271A-40	340	2	82.7	12.4	C 61
Sequence 40, Appli	US-08-449-315-40	340	2	82.7	12.4	C 62
Sequence 40, Appli	US-08-444-803-40	340	2	82.7	12.4	C 63
Sequence 40, Appli	US-08-449-043-40	340	2	82.7	12.4	C 64
Sequence 40, Appli	US-08-456-265A-40	340	2	82.7	12.4	C 65
Sequence 40, Appli	US-08-455-416-40	340	2	82.7	12.4	C 66
Sequence 40, Appli	US-08-455-244-40	340	2	82.7	12.4	C 67
Sequence 40, Appli	US-08-454-876-40	340	2	82.7	12.4	C 68
Sequence 40, Appli	US-08-457-362-40	340	2	82.7	12.4	C 69
Sequence 40, Appli	US-08-456-262-40	340	2	82.7	12.4	C 70
Sequence 40, Appli	US-08-456-240-40	340	2	82.7	12.4	C 71
Sequence 40, Appli	US-08-455-736-40	340	2	82.7	12.4	C 72
Sequence 40, Appli	US-08-971-217-40	340	2	82.7	12.4	C 73
Sequence 40, Appli	US-09-350-600-40	340	3	82.7	12.4	C 74
Sequence 40, Appli	US-09-906-234-40	340	3	82.7	12.4	C 75
Sequence 19122, A	US-09-513-999C-19122	433	3	82.7	12.4	C 76
Sequence 19046, A	US-09-621-976-19046	462	3	82.7	12.4	C 77
Sequence 4834, Ap	US-09-533-559-4834	462	3	82.7	12.4	C 78
Sequence 9941, Ap	US-08-975-316-26	493	2	82.7	12.4	C 79
Sequence 26, Appli	US-09-615-192A-26	508	2	82.7	12.4	C 80
Sequence 26, Appli	US-09-169-789-26	508	3	82.7	12.4	C 81
Sequence 26, Appli	US-09-270-767-28229	518	3	82.7	12.4	C 82
Sequence 1257, Ap	US-09-533-559-1257	588	3	82.7	12.4	C 83
Sequence 2593, Ap	US-09-533-559-2593	597	3	82.7	12.4	C 84
Sequence 70104, A	US-09-949-016-70104	601	3	82.7	12.4	C 85
Sequence 94191, A	US-09-949-016-94191	601	3	82.7	12.4	C 86
Sequence 16950, A	US-09-949-016-16950	601	3	82.7	12.4	C 87
Sequence 184368, A	US-09-949-016-184368	601	3	82.7	12.4	C 88
Sequence 205754, A	US-09-949-016-205754	601	3	82.7	12.4	C 89
Sequence 205755, A	US-09-949-016-205755	601	3	82.7	12.4	C 90
Sequence 205756, A	US-09-949-016-205756	601	3	82.7	12.4	C 91
Sequence 1176, Ap	US-09-598-401C-37	648	3	82.7	12.4	C 92
Sequence 37, Appli	US-09-533-559-4547	665	3	82.7	12.4	C 93
Sequence 4639, Ap	US-09-533-559-4639	678	3	82.7	12.4	C 94
Sequence 12849, A	US-09-270-767-12849	699	3	82.7	12.4	C 95

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:41:34 ; Search time 1705.5 Seconds

(without alignments)
411.496 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gcttcgtccgcttc 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	201	10	CG596662
2	15	100.0	229	10	CG670703
3	15	100.0	469	5	BW582202
4	15	100.0	486	5	BW574342
5	15	100.0	537	3	BM354327
6	15	100.0	661	9	BZ846224
7	15	100.0	672	6	CD427484
8	15	100.0	705	6	CB169687
9	15	100.0	718	6	CD462282
10	15	100.0	903	10	CNS01M9N
11	15	100.0	973	8	DR679944
12	15	100.0	1334	2	BG58140
13	15	100.0	1418	2	BF14115
14	14	93.3	86	6	CF003821
15	14	93.3	162	9	BZ712250
16	14	93.3	168	3	BJ683450
17	14	93.3	174	9	AZ086492
18	14	93.3	199	9	CC114390
19	14	93.3	264	5	BQ494805
20	14	93.3	269	9	AZ257720
21	14	93.3	298	1	AA793257
22	14	93.3	331	10	AG132185

BY173698	BY173698	359	5	BY173698
AA186624	AA186624	406	1	AA186624
BP526832	BP526832	407	3	BP526832
CZ114641	CZ114641	428	10	CZ114641
CV654226	CV654226	429	7	CV654226
BG489038	BG489038	451	2	BG489038
DR795082	DR795082	454	8	DR795082
AG268451	AG268451	469	10	AG268451
BJ534860	BJ534860	505	3	BJ534860
CV701467	CV701467	517	7	CV701467
AL929726	AL929726	521	1	AL929726
BH387066	BH387066	523	9	BH387066
BZ302204	BZ302204	523	9	BZ302204
AG976950	AG976950	526	10	AG976950
BH286581	BH286581	530	9	BH286581
BJ526748	BJ526748	535	3	BJ526748
AL126511	AL126511	542	11	AL126511
AO512515	AO512515	552	9	AO512515
CC713154	CC713154	557	9	CC713154
AG971437	AG971437	570	10	AG971437
CF002582	CF002582	579	6	CF002582
BG532424	BG532424	606	2	BG532424
CE451613	CE451613	612	10	CE451613
CF017551	CF017551	615	6	CF017551
BJ024639	BJ024639	617	3	BJ024639
DE039971	DE039971	623	2	DE039971
BH899238	BH899238	648	9	BH899238
CL972544	CL972544	651	10	CL972544
CK987950	CK987950	667	7	CK987950
CD650797	CD650797	675	6	CD650797
CV241577	CV241577	677	7	CV241577
DN586511	DN586511	680	8	DN586511
DN560688	DN560688	685	8	DN560688
CM013613	CM013613	685	10	CM013613
AG102835	AG102835	686	10	AG102835
CK724872	CK724872	709	8	CK724872
CC643278	CC643278	711	9	CC643278
BI872833	BI872833	712	3	BI872833
CG007385	CG007385	724	10	CG007385
CK186164	CK186164	725	7	CK186164
BI838675	BI838675	726	3	BI838675
CE270884	CE270884	729	10	CE270884
BI414805	BI414805	735	3	BI414805
BJ720211	BJ720211	741	3	BJ720211
BH666243	BH666243	756	9	BH666243
CG330968	CG330968	756	10	CG330968
CG268426	CG268426	782	10	CG268426
BZ733816	BZ733816	783	9	BZ733816
BH433362	BH433362	791	9	BH433362
BZ733812	BZ733812	796	9	BZ733812
BZ468768	BZ468768	798	9	BZ468768
BH899795	BH899795	799	9	BH899795
BU350535	BU350535	801	5	BU350535
AL273285	AL273285	807	11	AL273285
CC634234	CC634234	815	9	CC634234
CC695839	CC695839	817	9	CC695839
BE034274	BE034274	825	2	BE034274
BE283108	BE283108	841	2	BE283108
CG352157	CG352157	860	10	CG352157
CG610971	CG610971	862	9	CG610971
CG270251	CG270251	886	10	CG270251
AL225243	AL225243	893	11	AL225243
AG841932	AG841932	899	10	AG841932
AG883216	AG883216	899	10	AG883216
BF302129	BF302129	906	2	BF302129
CG818274	CG818274	907	10	CG818274
AG902696	AG902696	912	10	AG902696
CC453826	CC453826	920	10	CC453826
CC408230	CC408230	923	9	CC408230
CV967263	CV967263	944	8	CV967263
CC408225	CC408225	945	9	CC408225
CC610979	CC610979	947	9	CC610979

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 02:40:39 ; Search time 902.5 Seconds

(without alignments)
944.767 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaaggagca 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.to.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	100.0	52	1	AF318151 Staphyloc
C 2	15	100.0	58	1	AF318162 Staphyloc
C 3	15	100.0	69	1	AF311730 Staphyloc
C 4	15	100.0	301	1	AF456354 Staphyloc
C 5	15	100.0	325	1	AF456348 Staphyloc
C 6	15	100.0	325	1	AF456349 Staphyloc
C 7	15	100.0	326	3	AF467317 Unculture
C 8	15	100.0	327	3	AF467310 Unculture
C 9	15	100.0	330	3	AF467318 Unculture
C 10	15	100.0	363	1	ULU78937
C 11	15	100.0	418	1	AF456351 Staphyloc
C 12	15	100.0	435	1	AF456352 Staphyloc
C 13	15	100.0	442	1	AF456354 Staphyloc
C 14	15	100.0	464	1	AY227283 Staphyloc
C 15	15	100.0	464	1	AY688054 Staphyloc
C 16	15	100.0	464	1	AY688055 Staphyloc
C 17	15	100.0	464	1	AY688056 Staphyloc
C 18	15	100.0	464	1	AY688091 Staphyloc

C 19	15	100.0	464	1	AY688092 Staphyloc
C 20	15	100.0	464	1	AY688093 Staphyloc
C 21	15	100.0	464	1	AY688094 Staphyloc
C 22	15	100.0	464	1	AY688102 Staphyloc
C 23	15	100.0	464	1	AY688103 Staphyloc
C 24	15	100.0	464	1	AY688107 Staphyloc
C 25	15	100.0	464	1	AY688108 Staphyloc
C 26	15	100.0	464	1	AY688109 Staphyloc
C 27	15	100.0	464	1	AY894722 Staphyloc
C 28	15	100.0	464	3	AF078296 Grassland
C 29	15	100.0	476	1	AY126224 Staphyloc
C 30	15	100.0	483	1	AY126221 Staphyloc
C 31	15	100.0	492	3	AY957696 Unculture
C 32	15	100.0	493	1	AY227255 Staphyloc
C 33	15	100.0	493	1	AY227257 Staphyloc
C 34	15	100.0	494	1	AY227261 Staphyloc
C 35	15	100.0	494	1	AY227264 Staphyloc
C 36	15	100.0	495	1	AY227258 Staphyloc
C 37	15	100.0	495	1	AY227260 Staphyloc
C 38	15	100.0	495	1	AY227260 Staphyloc
C 39	15	100.0	497	1	AY126181 Staphyloc
C 40	15	100.0	498	1	AY227276 Staphyloc
C 41	15	100.0	503	1	AY879102 Staphyloc
C 42	15	100.0	504	1	AY126240 Staphyloc
C 43	15	100.0	505	3	AF467319 Unculture
C 44	15	100.0	506	1	AY421710 Staphyloc
C 45	15	100.0	507	3	AF467321 Unculture
C 46	15	100.0	508	1	AY126191 Staphyloc
C 47	15	100.0	508	1	AY126199 Staphyloc
C 48	15	100.0	508	1	AY126241 Staphyloc
C 49	15	100.0	510	1	AY227256 Staphyloc
C 50	15	100.0	510	1	AY227262 Staphyloc
C 51	15	100.0	511	1	AY126197 Staphyloc
C 52	15	100.0	512	1	AY126183 Staphyloc
C 53	15	100.0	512	1	AY126184 Staphyloc
C 54	15	100.0	512	1	AY126185 Staphyloc
C 55	15	100.0	512	1	AY126246 Staphyloc
C 56	15	100.0	512	1	AY126259 Staphyloc
C 57	15	100.0	513	1	AY426179 Staphyloc
C 58	15	100.0	513	1	AY126187 Staphyloc
C 59	15	100.0	514	1	AY126177 Staphyloc
C 60	15	100.0	514	1	AY126186 Staphyloc
C 61	15	100.0	515	1	AY126192 Staphyloc
C 62	15	100.0	515	1	AY126195 Staphyloc
C 63	15	100.0	515	1	AY126247 Staphyloc
C 64	15	100.0	516	1	AY126188 Staphyloc
C 65	15	100.0	516	1	AY126190 Staphyloc
C 66	15	100.0	516	1	AY126236 Staphyloc
C 67	15	100.0	516	1	AY126248 Staphyloc
C 68	15	100.0	516	1	AY126249 Staphyloc
C 69	15	100.0	517	1	AY126176 Staphyloc
C 70	15	100.0	517	1	AY126178 Staphyloc
C 71	15	100.0	517	1	AY126180 Staphyloc
C 72	15	100.0	517	1	AY126193 Staphyloc
C 73	15	100.0	517	1	AY126239 Staphyloc
C 74	15	100.0	518	1	AY126194 Staphyloc
C 75	15	100.0	518	1	AY126235 Staphyloc
C 76	15	100.0	518	1	AY126237 Staphyloc
C 77	15	100.0	519	1	AY126196 Staphyloc
C 78	15	100.0	519	1	AY126238 Staphyloc
C 79	15	100.0	520	1	AY126251 Staphyloc
C 80	15	100.0	529	10	BV391692 S243P6148
C 81	15	100.0	553	3	AY437986 Unculture
C 82	15	100.0	594	1	SSP36446 Staphyloc
C 83	15	100.0	652	10	BV277977 S232P6127
C 84	15	100.0	668	1	AY526654 Staphyloc
C 85	15	100.0	685	3	AF467320 Unculture
C 86	15	100.0	698	3	AF467321 Unculture
C 87	15	100.0	750	2	AF483074 Boltenia
C 88	15	100.0	751	1	AY211101 Staphyloc
C 89	15	100.0	771	1	SE16SRNB
C 90	15	100.0	771	1	SS16SRND
C 91	15	100.0	1112	15	BT000079 Arabidops

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:40:39 ; Search time 902.5 Seconds
(without alignments)
944.767 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gctctcgtccgttc 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5883142 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	6	AR438392 Sequence
2	15	100.0	80	6	A32047 DNA probe (
3	15	100.0	80	6	A32065 DNA probe (
4	15	100.0	113	6	AR358704 Sequence
5	15	100.0	113	6	AR540260 Sequence
6	15	100.0	305	6	AR358257 Sequence
7	15	100.0	305	6	AR539813 Sequence
8	15	100.0	305	1	DO056338 Sequence
9	15	100.0	356	6	AR358175 Sequence
10	15	100.0	356	6	AR358731 Sequence
11	15	100.0	400	6	AR357432 Sequence
12	15	100.0	400	6	AR357471 Sequence
13	15	100.0	400	6	AR357515 Sequence
14	15	100.0	400	6	AR357684 Sequence
15	15	100.0	400	6	AR357710 Sequence
16	15	100.0	400	6	AR358044 Sequence
17	15	100.0	400	6	AR358988 Sequence
18	15	100.0	400	6	AR539027 Sequence

c 19	15	100.0	400	6	AR539071 Sequence
20	15	100.0	400	6	AR539240 Sequence
21	15	100.0	400	6	AR539266 Sequence
c 22	15	100.0	400	6	AR539600 Sequence
c 23	15	100.0	419	1	SSP489358
c 24	15	100.0	464	1	AY688031
c 25	15	100.0	464	1	AY688032
c 26	15	100.0	464	1	AY688033
c 27	15	100.0	464	1	AY688034
c 28	15	100.0	464	1	AY688035
c 29	15	100.0	471	1	UBA295368
c 30	15	100.0	481	1	UBA295367
c 31	15	100.0	495	1	AY266427
c 32	15	100.0	503	3	AY939432
c 33	15	100.0	505	3	AY126146
c 34	15	100.0	505	3	AY939176
c 35	15	100.0	506	3	AY939175
c 36	15	100.0	506	3	AY939188
c 37	15	100.0	506	3	AY939293
c 38	15	100.0	506	3	AY939297
c 39	15	100.0	507	3	AY939174
c 40	15	100.0	507	3	AY939187
c 41	15	100.0	507	3	AY939303
c 42	15	100.0	508	3	AY939193
c 43	15	100.0	508	3	AY939449
c 44	15	100.0	509	3	AY939452
c 45	15	100.0	510	1	AY126144
c 46	15	100.0	510	3	AY939430
c 47	15	100.0	510	3	AY939433
c 48	15	100.0	510	3	AY939445
c 49	15	100.0	511	3	AY939437
c 50	15	100.0	511	3	AY939439
c 51	15	100.0	511	3	AY939441
c 52	15	100.0	511	3	AY939444
c 53	15	100.0	512	3	AY939435
c 54	15	100.0	513	3	AY939436
c 55	15	100.0	513	3	AY939447
c 56	15	100.0	514	3	AY939438
c 57	15	100.0	515	1	AY126148
c 58	15	100.0	515	1	AY305000S2
c 59	15	100.0	516	1	AY126147
60	15	100.0	517	1	AY126145
c 61	15	100.0	535	1	AY504461
c 62	15	100.0	579	6	AR535517
63	15	100.0	579	6	AR537073
c 64	15	100.0	589	6	AR537512
c 65	15	100.0	589	6	AR539068
c 66	15	100.0	747	8	HS4330262
c 67	15	100.0	757	1	AF343958
c 68	15	100.0	771	1	SH16SRNRD
c 69	15	100.0	798	3	AY805987
c 70	15	100.0	799	3	AY805992
c 71	15	100.0	799	3	AY806277
c 72	15	100.0	807	3	AY806472
c 73	15	100.0	816	3	AY806200
c 74	15	100.0	816	3	AY806674
c 75	15	100.0	834	3	AY807213
c 76	15	100.0	834	3	AY807396
c 77	15	100.0	840	1	AY437618
c 78	15	100.0	849	3	AY807545
c 79	15	100.0	850	3	AY807542
c 80	15	100.0	861	3	AY807554
c 81	15	100.0	870	3	AY807387
c 82	15	100.0	958	1	AY859409
c 83	15	100.0	1141	1	AF076030
c 84	15	100.0	1171	6	AR357421
c 85	15	100.0	1171	6	AR538977
c 86	15	100.0	1290	6	AR357076
c 87	15	100.0	1290	6	AR538632
c 88	15	100.0	1437	1	SA16S
c 89	15	100.0	1442	1	AF015929
c 90	15	100.0	1476	1	ST416SRR01
c 91	15	100.0	1476	1	ST416SRR02

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:39:02 ; Search time 244.5 Seconds
(without alignments)
408.877 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gcttcgtccgttc 15

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

N_Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	12	ADM86613 S. aureus
2	15	100.0	15	14	ADX26645
3	15	100.0	15	14	AEAS9581 Staphyloc
4	15	100.0	15	14	ADX26648 Staphyloc
5	15	100.0	15	14	ADX26654 Staphyloc
6	15	100.0	15	14	ADX26653 Staphyloc
7	15	100.0	15	12	ADX26653 Staphyloc
8	15	100.0	113	2	AAV79133 Staphyloc
9	15	100.0	305	2	AAV78604 Staphyloc
10	15	100.0	356	2	AAV78604 Staphyloc
11	15	100.0	360	13	AAV99473 Staphyloc
12	15	100.0	400	2	AAV78473 Staphyloc
13	15	100.0	400	2	AAV77944 Staphyloc
14	15	100.0	400	2	AAV78113 Staphyloc
15	15	100.0	400	2	AAV7861 Staphyloc
16	15	100.0	400	2	AAV78139 Staphyloc
17	15	100.0	400	2	AAV77900 Staphyloc
18	15	100.0	579	2	AAV75946 Staphyloc
19	15	100.0	589	2	AAV77941 Staphyloc

C	20	15	100.0	1171	2	AAV77850	Aav77850 Staphyloc
C	21	15	100.0	1239	13	ADS48229	AdS48229 Bacterial
C	22	15	100.0	1290	13	AAV77505	Aav77505 Staphyloc
C	23	15	100.0	1442	6	ABS71606	Abs71606 Staphyloc
C	24	15	100.0	1484	5	AAS11026	Aas11026 Staphyloc
C	25	15	100.0	1555	2	AAT29142	Aat29142 rRNA gene
C	26	15	100.0	1555	2	AAV24294	Aav24294 Staphyloc
C	27	15	100.0	1555	6	AAK99056	Aak99056 DNA of th
C	28	15	100.0	1555	6	AAK99099	Aak99099 DNA encod
C	29	15	100.0	1555	9	ADB16301	AdB16301 Cleavase
C	30	15	100.0	1555	10	ADB61676	AdB61676 16S rRNA
C	31	15	100.0	1555	10	ADC02549	AdC02549 S. aureus
C	32	15	100.0	1555	14	ADM94447	AdM94447 Prolifera
C	33	15	100.0	1555	14	ADM94575	AdM94575 Prolifera
C	34	15	100.0	1555	14	ADM94604	AdM94604 Prolifera
C	35	15	100.0	1555	14	ADM94509	AdM94509 Prolifera
C	36	15	100.0	2209	2	AAV77863	Aav77863 Staphyloc
C	37	15	100.0	5029	14	ADM94255	AdM94255 Staphyloc
C	38	15	100.0	5134	14	ADM94228	AdM94228 Staphyloc
C	39	15	100.0	5648	14	ADM94202	AdM94202 Staphyloc
C	40	15	100.0	7291	14	ADM94182	AdM94182 Staphyloc
C	41	15	100.0	30246	2	AAV74367	Aav74367 Staphyloc
C	42	14	93.3	19	12	ADO18380	AdO18380 Analytica
C	43	14	93.3	19	12	ADO18671	AdO18671 Analytica
C	44	14	93.3	19	12	ADO18243	AdO18243 Analytica
C	45	14	93.3	19	12	ADO18529	AdO18529 Analytica
C	46	14	93.3	24	3	AAZ24183	Aaz24183 Bacterial
C	47	14	93.3	24	3	AAZ24171	Aaz24171 Bacterial
C	48	14	93.3	589	10	ADK55636	AdK55636 Plant DNA
C	49	14	93.3	649	10	ADK59378	AdK59378 Plant DNA
C	50	14	93.3	939	8	ACA47616	AcA47616 Prokaryot
C	51	14	93.3	1014	13	ADT16297	AdT16297 Plant CDN
C	52	14	93.3	1290	4	AAS56287	Aas56287 Salmoneil
C	53	14	93.3	1290	8	ACA52051	AcA52051 Prokaryot
C	54	14	93.3	1290	8	ACA51053	AcA51053 Prokaryot
C	55	14	93.3	1500	10	ADK60148	AdK60148 Plant DNA
C	56	14	93.3	1593	4	ABL25547	AbL25547 Drosophil
C	57	14	93.3	2744	13	ADS54871	AdS54871 Bacterial
C	58	14	93.3	2744	13	ADS54872	AdS54872 Bacterial
C	59	14	93.3	3774	4	ABL25546	AbL25546 Drosophil
C	60	13.4	89.3	25	9	ACI73669	AcI73669 Human mic
C	61	13.4	89.3	43	14	ADX26652	AdX26652 Staphyloc
C	62	13.4	89.3	43	14	ADX26651	AdX26651 Staphyloc
C	63	13.4	89.3	43	14	ADX26647	AdX26647 Staphyloc
C	64	13.4	89.3	129	2	AAV79101	Aav79101 Staphyloc
C	65	13.4	89.3	303	12	ADJ71864	AdJ71864 Human DNA
C	66	13.4	89.3	303	12	ADJ71861	AdJ71861 Human DNA
C	67	13.4	89.3	303	12	ADJ71865	AdJ71865 Human DNA
C	68	13.4	89.3	303	12	ADJ71863	AdJ71863 Human DNA
C	69	13.4	89.3	449	9	ACH39588	AcH39588 Human foe
C	70	13.4	89.3	538	6	ABZ34920	AbZ34920 Human gen
C	71	13.4	89.3	587	6	ABZ34920	AbZ34920 Human gen
C	72	13.4	89.3	609	14	ACL72402	AcL72402 M. xanthu
C	73	13.4	89.3	763	3	AAC39828	Aac39828 Arabidops
C	74	13.4	89.3	807	4	ABL30209	AbL30209 Drosophil
C	75	13.4	89.3	855	13	ADT42391	AdT42391 Bacterial
C	76	13.4	89.3	1014	10	ADG73022	AdG73022 DNA encod
C	77	13.4	89.3	1014	10	ADL12077	AdL12077 Pseudomon
C	78	13.4	89.3	1056	6	ABK75036	AbK75036 Bacillus
C	79	13.4	89.3	1101	12	ADJ71868	AdJ71868 Human DNA
C	80	13.4	89.3	1116	12	ADJ71867	AdJ71867 Human DNA
C	81	13.4	89.3	1134	12	ADJ71866	AdJ71866 Human DNA
C	82	13.4	89.3	1167	12	ADJ71869	AdJ71869 Human DNA
C	83	13.4	89.3	1179	12	ADJ71872	AdJ71872 Human DNA
C	84	13.4	89.3	1179	12	ADJ71871	AdJ71871 Human DNA
C	85	13.4	89.3	1179	12	ADJ71862	AdJ71862 Human DNA
C	86	13.4	89.3	1179	12	ADJ71870	AdJ71870 Human DNA
C	87	13.4	89.3	1197	13	ADS47832	AdS47832 Bacterial
C	88	13.4	89.3	1221	13	ADT45063	AdT45063 Bacterial
C	89	13.4	89.3	1260	8	ACA24877	AcA24877 Prokaryot
C	90	13.4	89.3	1341	6	ABQ69254	AbQ69254 Listeria
C	91	13.4	89.3	1356	6	ABQ67804	AbQ67804 Listeria
C	92	13.4	89.3	1362	3	AAA59628	Aaa59628 Nucleotid

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:15:47 ; Search time 282 Seconds
(without alignments)
116.622 Million cell updates/sec

Title: US-10-804-470-1

Perfect score: 15

Sequence: 1 gcttcgtcgttc 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 500 summaries

Database :

Published Applications NA New:
1: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
11: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-10-631-289-2	Sequence 2, Appli
C 2	15	100.0	1555	US-11-198-746-160	Sequence 160, App
C 3	15	100.0	1555	US-11-198-746-160	Sequence 160, App
C 4	15	100.0	1555	US-11-198-746-160	Sequence 160, App
C 5	13.4	89.3	568	US-09-925-065A-751129	Sequence 751129,
C 6	13.4	89.3	600	US-10-750-185-2543	Sequence 2543, Ap
C 7	13.4	89.3	600	US-10-750-185-2543	Sequence 2543, Ap
C 8	13.4	89.3	793	US-10-750-185-43321	Sequence 43321, A
C 9	13.4	89.3	793	US-10-750-185-43321	Sequence 43321, A
C 10	13.4	89.3	2727	US-10-821-234-415	Sequence 43321, A
C 11	13.4	89.3	5259	US-11-181-330-1	Sequence 415, Appl
C 12	13.4	89.3	5382	US-11-136-527-2050	Sequence 2050, Ap
C 13	13.4	89.3	6126	US-10-775-169-286	Sequence 286, App
C 14	13.4	89.3	14896	US-11-000-147-243	Sequence 243, App
C 15	13.4	89.3	14896	US-11-000-147-243	Sequence 243, App
C 16	13.4	89.3	14896	US-11-000-147-243	Sequence 243, App
C 17	13.4	89.3	173120	US-11-076-427A-31	Sequence 946, Appl
C 18	13.4	89.3	182303	US-11-114-798-55	Sequence 55, Appl
C 19	13	86.7	548	US-11-121-086-45	Sequence 45, Appl
C 20	13	86.7	80345	US-09-925-065A-46850	Sequence 46850, A
				US-11-124-367A-5022	Sequence 5022, Ap

13	86.7	81706	8	US-10-995-561-13417	Sequence 13417, A
13	86.7	1125000	8	US-10-995-561-13286	Sequence 13286, A
22	82.7	50	12	US-11-175-859-28227	Sequence 28227, A
23	82.7	86	8	US-10-310-914A-13940	Sequence 13940, A
24	82.7	326	6	US-09-925-065A-448010	Sequence 448010,
C 25	82.7	336	6	US-09-925-065A-797025	Sequence 797025,
C 26	82.7	336	6	US-09-925-065A-797025	Sequence 797025,
C 27	82.7	363	6	US-09-925-065A-850758	Sequence 850758,
C 28	82.7	409	6	US-09-925-065A-638012	Sequence 638012,
C 29	82.7	415	6	US-09-925-065A-795181	Sequence 795181,
C 30	82.7	417	12	US-11-136-527-15	Sequence 15, Appl
C 31	82.7	417	12	US-11-136-527-15	Sequence 15, Appl
C 32	82.7	419	6	US-09-925-065A-850759	Sequence 850759,
C 33	82.7	429	6	US-09-925-065A-448011	Sequence 448011,
C 34	82.7	458	6	US-09-925-065A-448008	Sequence 448008,
C 35	82.7	458	6	US-09-925-065A-124697	Sequence 124697,
C 36	82.7	452	6	US-09-925-065A-954872	Sequence 954872,
C 37	82.7	494	6	US-09-925-065A-543499	Sequence 543499,
C 38	82.7	494	6	US-09-925-065A-795180	Sequence 795180,
C 39	82.7	494	6	US-09-925-065A-795182	Sequence 795182,
C 40	82.7	494	6	US-09-925-065A-851789	Sequence 851789,
C 41	82.7	495	6	US-09-925-065A-946592	Sequence 946592,
C 42	82.7	503	6	US-09-925-065A-850757	Sequence 850757,
C 43	82.7	510	6	US-09-925-065A-797024	Sequence 797024,
C 44	82.7	510	6	US-09-925-065A-797026	Sequence 797026,
C 45	82.7	511	6	US-09-925-065A-111308	Sequence 111308,
C 46	82.7	511	6	US-09-925-065A-232256	Sequence 232256,
C 47	82.7	533	6	US-09-925-065A-665062	Sequence 665062,
C 48	82.7	554	6	US-09-925-065A-435304	Sequence 435304,
C 49	82.7	561	6	US-09-925-065A-404249	Sequence 404249,
C 50	82.7	566	6	US-09-925-065A-316047	Sequence 316047,
C 51	82.7	570	6	US-09-925-065A-232257	Sequence 232257,
C 52	82.7	572	6	US-09-925-065A-448012	Sequence 448012,
C 53	82.7	585	6	US-09-925-065A-108088	Sequence 108088,
C 54	82.7	586	6	US-09-925-065A-787292	Sequence 787292,
C 55	82.7	586	6	US-09-925-065A-813086	Sequence 813086,
C 56	82.7	589	6	US-09-925-065A-341380	Sequence 341380,
C 57	82.7	596	6	US-09-925-065A-258230	Sequence 258230,
C 58	82.7	596	6	US-09-925-065A-641653	Sequence 641653,
C 59	82.7	603	6	US-09-925-065A-939582	Sequence 939582,
C 60	82.7	603	6	US-09-925-065A-939583	Sequence 939583,
C 61	82.7	606	6	US-09-925-065A-921523	Sequence 921523,
C 62	82.7	606	6	US-09-925-065A-921524	Sequence 921524,
C 63	82.7	632	6	US-09-925-065A-444395	Sequence 444395,
C 64	82.7	632	6	US-09-925-065A-444396	Sequence 444396,
C 65	82.7	637	6	US-09-925-065A-795609	Sequence 795609,
C 66	82.7	646	6	US-09-925-065A-6710	Sequence 6710, Ap
C 67	82.7	646	6	US-09-925-065A-6710	Sequence 6710, Ap
C 68	82.7	646	6	US-09-925-065A-6711	Sequence 6711, Ap
C 69	82.7	646	6	US-09-925-065A-6712	Sequence 6712, Ap
C 70	82.7	646	6	US-09-925-065A-6713	Sequence 6713, Ap
C 71	82.7	648	8	US-10-927-641-37	Sequence 37, Appl
C 72	82.7	662	6	US-09-925-065A-801292	Sequence 801292,
C 73	82.7	662	6	US-09-925-065A-801293	Sequence 801293,
C 74	82.7	662	6	US-09-925-065A-801294	Sequence 801294,
C 75	82.7	662	6	US-09-925-065A-855090	Sequence 855090,
C 76	82.7	677	6	US-09-925-065A-112693	Sequence 112693,
C 77	82.7	681	6	US-09-925-065A-680454	Sequence 680454,
C 78	82.7	681	6	US-09-925-065A-782688	Sequence 782688,
C 79	82.7	746	8	US-10-750-185-56409	Sequence 56409, A
C 80	82.7	746	8	US-10-750-185-56409	Sequence 56409, A
C 81	82.7	806	6	US-09-925-065A-17024	Sequence 17024, A
C 82	82.7	806	6	US-09-925-065A-17025	Sequence 17025, A
C 83	82.7	806	6	US-09-925-065A-17026	Sequence 17026, A
C 84	82.7	812	6	US-09-925-065A-84823	Sequence 84823, A
C 85	82.7	827	8	US-10-750-185-35055	Sequence 35055, A
C 86	82.7	827	8	US-10-750-185-35055	Sequence 35055, A
C 87	82.7	1039	8	US-10-750-623-45107	Sequence 45107, A
C 88	82.7	1039	8	US-10-750-623-45107	Sequence 45107, A
C 89	82.7	1155	8	US-10-750-185-29185	Sequence 29185, A
C 90	82.7	1155	8	US-10-750-623-29185	Sequence 29185, A
C 91	82.7	1465	12	US-11-076-733-17	Sequence 17, Appl
C 92	82.7	1511	6	US-09-925-065A-43144	Sequence 43144, A
C 93	82.7	1511	6	US-09-925-065A-43145	Sequence 43145, A

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:39:02 ; Search time 244.5 Seconds
(without alignments)
408.677 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaaggagcaaa 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

N_Geneseq_21.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	ADX26646	Adx26646 Probe B f
2	15	100.0	43	ADX26652	Adx26652 Staphyloc
3	15	100.0	43	ADX26651	Adx26651 Staphyloc
4	15	100.0	43	ADX26649	Adx26649 Staphyloc
5	15	100.0	43	ADX26647	Adx26647 Staphyloc
6	15	100.0	43	ADX26650	Adx26650 Staphyloc
7	15	100.0	1122	3 AAC36196	Aac36196 Arabidops
8	15	100.0	1234	3 AAC37820	Aac37820 Arabidops
9	15	100.0	2102	4 AAI68993	Aai68993 Prostata
10	14	93.3	41	2 AAV39906	Aav39906 Streptoco
11	14	93.3	41	6 ABO85067	Abg85067 Streptoco
12	14	93.3	41	10 ADC45470	Adc45470 S. pneumo
13	14	93.3	172	3 AAC21883	Aac21883 Human sec
14	14	93.3	223	5 AAS33655	Aas33655 Human cdn
15	14	93.3	339	9 ADA32201	Ada32201 DNA encod
16	14	93.3	373	5 ABV17168	Abv17168 Human pro
17	14	93.3	378	8 ABX42264	Abx42264 Bovine ES
18	14	93.3	434	5 ADI72025	Adi72025 Human ova
19	14	93.3	434	5 ADL37174	Adl37174 Human ova

20	14	93.3	503	5	ABV46963	Abv46963 Human pro
21	14	93.3	525	10	ADE78377	Ade78377 Endometri
22	14	93.3	525	10	ADE78378	Ade78378 Endometri
23	14	93.3	578	5	AAS34736	Aas34736 Human DNA
24	14	93.3	578	5	AAS34737	Aas34737 Human DNA
25	14	93.3	578	5	AAS34738	Aas34738 Human DNA
26	14	93.3	585	5	ADL43558	Adl43558 Human ova
27	14	93.3	784	2	AAV27405	Aav27405 Streptoco
28	14	93.3	784	6	ABQ84873	Abq84873 S. pneumo
29	14	93.3	784	10	ADC45244	Adc45244 S. pneumo
30	14	93.3	794	13	ADN33184	Adn33184 Human tra
31	14	93.3	981	13	ADT20022	Adt20022 Plant cdn
32	14	93.3	1116	6	ABN90844	Abn90844 Staphyloc
33	14	93.3	1116	13	ADS00985	Ads00985 Staphyloc
34	14	93.3	1134	13	ADR93082	Adr93082 Novel S.
35	14	93.3	1134	13	ADK46071	Adk46071 Streptoco
36	14	93.3	1134	14	AEA56952	Aea56952 Streptoco
37	14	93.3	1230	13	ADN33185	Adn33185 Human tra
38	14	93.3	1410	6	ABN81334	Abn81334 Physcomit
39	14	93.3	1410	8	ABX16241	Abx16241 P. patens
40	14	93.3	1689	10	ABX06328	Abx06328 S. pneumo
41	14	93.3	1692	3	AAA05463	Aaa05463 Streptoco
42	14	93.3	1693	3	AAA05462	Aaa05462 Streptoco
43	14	93.3	2147	14	AE867769	Aeb7769 Rice geno
44	14	93.3	2188	12	ADN05369	Adn05369 Antipsori
45	14	93.3	3068	13	ADT19986	Adt19986 Plant cdn
46	14	93.3	3135	2	AAV82049	Aav82049 Polynucle
47	14	93.3	3135	2	AAV82048	Aav82048 S. pneumo
48	14	93.3	3135	2	AAI16687	Aax16687 Streptoco
49	14	93.3	3135	2	AAI16688	Aax16688 Streptoco
50	14	93.3	3135	4	AAH47451	Aah47451 S. pneumo
51	14	93.3	3135	4	AAH47452	Aah47452 S. pneumo
52	14	93.3	3135	9	ADA14564	Ada14564 DNA encod
53	14	93.3	3135	9	ADA14561	Ada14561 DNA encod
54	14	93.3	4008	4	ABL20178	AbL20178 Drosophila
55	14	93.3	4085	14	AEA22587	Aea22587 TRP chann
56	14	93.3	4085	14	AE886304	Aeb86304 Nucleotid
57	14	93.3	4174	6	ABZ35297	Abz35297 Human gen
58	14	93.3	4345	5	AAS86250	Aas86250 DNA encod
59	14	93.3	4361	10	ABT42027	Abt42027 Toxicity
60	14	93.3	4361	12	ADP72826	Adp72826 Renal tox
61	14	93.3	5034	12	ADP76091	Adp76091 Genomic D
62	14	93.3	5217	4	ABL21514	AbL21514 Drosophila
63	14	93.3	5554	12	ADN04185	Adn04185 Antipsori
64	14	93.3	5555	6	ABZ35675	Abz35675 Human gen
65	14	93.3	6317	8	ACC47865	Acc47865 P. obesus
66	14	93.3	10785	4	ABA07367	Abao7367 Human pan
67	14	93.3	10785	4	AAK91098	Aak91098 Human dig
68	14	93.3	10785	4	AAK65411	Aak65411 Human imm
69	14	93.3	10785	5	AAS30060	Aas30060 Human lun
70	14	93.3	10785	10	ADB33397	Adb33397 Human nov
71	14	93.3	12729	5	AAF97873	Aaf97873 Human neu
72	14	93.3	13315	4	ABA07371	Abao7371 Human pan
73	14	93.3	13315	4	AAK91102	Aak91102 Human dig
74	14	93.3	13315	4	AAK65415	Aak65415 Human imm
75	14	93.3	13315	5	AAS30064	Aas30064 Human lun
76	14	93.3	13315	10	ADB33401	Adb33401 Human nov
77	14	93.3	13926	2	AAV52138	Aav52138 Streptoco
78	14	93.3	20261	4	ABA07368	Abao7368 Human pan
79	14	93.3	20261	4	AAK91099	Aak91099 Human dig
80	14	93.3	20261	4	AAK65412	Aak65412 Human imm
81	14	93.3	20261	5	AAS30061	Aas30061 Human lun
82	14	93.3	20261	10	ADB33398	Adb33398 Human nov
83	14	93.3	25464	2	AAV57274	Aav57274 Human fla
84	14	93.3	84805	14	ABE39165	Aeb39165 L. pneumo
85	14	93.3	110000	10	ADE11169	Adel1169 L. pneumo
86	14	93.3	110000	10	ABE56454	Abes56454 L. pneumo
87	14	93.3	110000	10	ABE39175	Abes39175 L. pneumo
88	14	93.3	110000	14	ABE42401	Abes42401 L. pneumo
89	14	93.3	110000	14	ABE42736	Abes42736 L. pneumo
90	14	93.3	125910	3	AC64370	Aac64370 Human KCN
91	14	93.3	150351	13	ABD33360	Abd33360 Murine ca
92	14	93.3	185548	13	ADV34986	Adv34986 Murine cd

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:53:29 ; Search time 118.5 Seconds
(without alignments)
225.008 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaagagagcaa 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
 - 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
 - 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
 - 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
 - 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
 - 6: /cgn2_6/prodata/1/ina/PCUS COMB.seq.*
 - 7: /cgn2_6/prodata/1/ina/pp COMB.seq.*
 - 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
 - 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14	93.3	41	3	US-08-961-083-389
C 2	14	93.3	41	3	US-09-536-784-389
C 3	14	93.3	41	3	US-09-765-271-389
C 4	14	93.3	41	3	US-09-765-272A-389
C 5	14	93.3	172	3	US-09-513-998C-25958
C 6	14	93.3	339	3	US-09-328-352-3488
C 7	14	93.3	601	3	US-09-949-016-27145
C 8	14	93.3	601	3	US-09-949-016-63597
C 9	14	93.3	601	3	US-09-949-016-63598
C 10	14	93.3	601	3	US-09-949-016-103753
C 11	14	93.3	784	3	US-08-961-083-163
C 12	14	93.3	784	3	US-09-536-784-163
C 13	14	93.3	784	3	US-09-765-271-163
C 14	14	93.3	784	3	US-09-765-272A-163
C 15	14	93.3	1116	3	US-09-134-001C-307
C 16	14	93.3	1134	3	US-09-583-110-2586
C 17	14	93.3	1134	3	US-09-107-433-117
C 18	14	93.3	1410	3	US-09-828-302-10
C 19	14	93.3	1692	3	US-09-769-787-235
C 20	14	93.3	1692	3	US-09-769-787-236
C 21	14	93.3	3135	3	US-09-321-276-1
C 22	14	93.3	3135	3	US-09-321-276-3
C 23	14	93.3	3135	3	US-08-916-481-1
C 24	14	93.3	3135	3	US-08-916-481-4

25	14	93.3	3405	3	US-09-949-016-2869	Sequence 2869, Ap
26	14	93.3	3825	2	US-08-737-597-2	Sequence 2, Appli
27	14	93.3	4085	3	US-09-949-016-469	Sequence 469, App
28	14	93.3	13926	3	US-08-961-527-5	Sequence 5, Appli
29	14	93.3	25464	3	US-09-326-480A-4	Sequence 4, Appli
30	14	93.3	34261	3	US-09-949-016-14611	Sequence 14611, A
31	14	93.3	85368	3	US-09-949-016-12211	Sequence 12211, A
32	14	93.3	98439	3	US-09-949-016-13597	Sequence 13597, A
33	14	93.3	360470	3	US-09-949-016-13173	Sequence 13173, A
C 34	13.4	89.3	163	3	US-09-113-294A-700	Sequence 700, App
C 35	13.4	89.3	188	3	US-09-513-998C-27410	Sequence 27410, A
C 36	13.4	89.3	258	3	US-09-107-433-1851	Sequence 1851, Ap
C 37	13.4	89.3	601	3	US-09-949-016-33580	Sequence 33580, A
C 38	13.4	89.3	601	3	US-09-949-016-33581	Sequence 33581, A
C 39	13.4	89.3	601	3	US-09-949-016-48061	Sequence 48061, A
C 40	13.4	89.3	601	3	US-09-949-016-68083	Sequence 68083, A
C 41	13.4	89.3	601	3	US-09-949-016-80541	Sequence 80541, A
C 42	13.4	89.3	601	3	US-09-949-016-80542	Sequence 80542, A
C 43	13.4	89.3	601	3	US-09-949-016-83198	Sequence 83198, A
C 44	13.4	89.3	601	3	US-09-949-016-83290	Sequence 83290, A
C 45	13.4	89.3	601	3	US-09-949-016-122281	Sequence 122281, A
C 46	13.4	89.3	601	3	US-09-949-016-128690	Sequence 128690, A
C 47	13.4	89.3	601	3	US-09-949-016-129009	Sequence 129009, A
C 48	13.4	89.3	601	3	US-09-949-016-159901	Sequence 159901, A
C 49	13.4	89.3	601	3	US-09-949-016-189468	Sequence 189468, A
C 50	13.4	89.3	601	3	US-09-949-016-193552	Sequence 193552, A
C 51	13.4	89.3	601	3	US-09-949-016-196236	Sequence 196236, A
C 52	13.4	89.3	601	3	US-09-949-016-196237	Sequence 196237, A
C 53	13.4	89.3	601	3	US-09-949-016-196716	Sequence 196716, A
C 54	13.4	89.3	601	3	US-09-949-003-8884	Sequence 8884, Ap
C 55	13.4	89.3	601	3	US-09-949-003-8885	Sequence 8885, Ap
C 56	13.4	89.3	601	3	US-09-949-002-8886	Sequence 8886, Ap
C 57	13.4	89.3	659	3	US-09-533-555-7125	Sequence 7125, Ap
C 58	13.4	89.3	795	3	US-09-533-559-1918	Sequence 1918, Ap
C 59	13.4	89.3	1167	3	US-09-134-001C-983	Sequence 983, App
C 60	13.4	89.3	1617	3	US-09-413-304-8	Sequence 8, Appli
C 61	13.4	89.3	1617	3	US-09-817-856-8	Sequence 8, Appli
C 62	13.4	89.3	1718	3	US-09-215-450-17	Sequence 17, Appli
C 63	13.4	89.3	1890	3	US-09-248-796A-1325	Sequence 1325, Ap
C 64	13.4	89.3	2061	3	US-09-653-839-7	Sequence 7, Appli
C 65	13.4	89.3	2061	3	US-10-202-619-7	Sequence 7, Appli
C 66	13.4	89.3	2109	3	US-09-653-839-5	Sequence 5, Appli
C 67	13.4	89.3	2109	3	US-10-202-619-5	Sequence 5, Appli
C 68	13.4	89.3	2172	3	US-09-653-839-3	Sequence 3, Appli
C 69	13.4	89.3	2172	3	US-10-202-619-3	Sequence 3, Appli
C 70	13.4	89.3	2220	3	US-09-653-839-1	Sequence 1, Appli
C 71	13.4	89.3	2220	3	US-10-202-619-1	Sequence 1, Appli
C 72	13.4	89.3	2341	3	US-09-949-016-4080	Sequence 4080, Ap
C 73	13.4	89.3	2387	3	US-08-961-527-56	Sequence 56, Appli
C 74	13.4	89.3	2492	3	US-09-949-016-5560	Sequence 5560, Ap
C 75	13.4	89.3	2806	3	US-09-653-839-9	Sequence 9, Appli
C 76	13.4	89.3	2806	3	US-10-202-619-9	Sequence 9, Appli
C 77	13.4	89.3	2817	3	US-10-104-047-1687	Sequence 1687, Ap
C 78	13.4	89.3	3250	3	US-09-949-016-800	Sequence 800, App
C 79	13.4	89.3	3754	3	US-09-561-709B-6	Sequence 6, Appli
C 80	13.4	89.3	3818	3	US-09-949-016-5445	Sequence 5445, Ap
C 81	13.4	89.3	4286	3	US-09-413-304-7	Sequence 7, Appli
C 82	13.4	89.3	4286	3	US-09-817-856-7	Sequence 7, Appli
C 83	13.4	89.3	4289	3	US-09-949-016-627	Sequence 627, App
C 84	13.4	89.3	5874	3	US-09-561-709B-2	Sequence 2, Appli
C 85	13.4	89.3	10106	3	US-09-949-016-17187	Sequence 17187, A
C 86	13.4	89.3	11667	3	US-09-949-016-13934	Sequence 13934, A
C 87	13.4	89.3	14565	3	US-09-949-016-16620	Sequence 16620, A
C 88	13.4	89.3	18471	3	US-09-949-016-14288	Sequence 14288, A
C 89	13.4	89.3	25190	3	US-09-949-016-15906	Sequence 15906, A
C 90	13.4	89.3	25559	3	US-09-949-016-16707	Sequence 16707, A
C 91	13.4	89.3	27120	3	US-09-949-016-15822	Sequence 15822, A
C 92	13.4	89.3	27120	3	US-09-949-016-16210	Sequence 16210, A
C 93	13.4	89.3	27933	3	US-09-949-016-12369	Sequence 12369, A
C 94	13.4	89.3	29569	3	US-09-949-016-15875	Sequence 15875, A
C 95	13.4	89.3	29960	3	US-09-949-016-11978	Sequence 11978, A
C 96	13.4	89.3	30054	3	US-09-949-016-16100	Sequence 16100, A
C 97	13.4	89.3	30291	3	US-09-949-016-12875	Sequence 12875, A

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:15:47 ; Search time 282 Seconds
(without alignments)
116.622 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 attctaaagagca 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications_NA_New.*

1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	93.3	25	12	US-11-136-527-110483
C 2	14	93.3	25	12	US-11-136-527-110485
C 3	14	93.3	25	12	US-11-136-527-110492
C 4	14	93.3	25	12	US-11-136-527-110503
C 5	14	93.3	25	12	US-11-136-527-110504
C 6	14	93.3	25	12	US-11-136-527-110505
C 7	14	93.3	25	12	US-11-136-527-110514
C 8	14	93.3	25	12	US-11-136-527-110514
C 9	14	93.3	25	12	US-11-136-527-112762
C 10	14	93.3	25	12	US-11-136-527-312778
C 11	14	93.3	25	12	US-11-136-527-312781
C 12	14	93.3	25	12	US-11-136-527-312785
C 13	14	93.3	25	12	US-11-136-527-312789
C 14	14	93.3	25	12	US-09-925-065A-95610
C 15	14	93.3	520	6	US-09-925-065A-404803
C 16	14	93.3	543	6	US-09-925-065A-340164
C 17	14	93.3	559	6	US-09-925-065A-156850
C 18	14	93.3	587	6	US-09-925-065A-457748
C 19	14	93.3	600	12	US-11-136-527-6628
C 20	14	93.3	609	6	US-09-925-065A-835726

21	14	93.3	611	6	US-09-925-065A-383746	Sequence 383746,
22	14	93.3	611	6	US-09-925-065A-383747	Sequence 383747,
23	14	93.3	611	6	US-09-925-065A-383748	Sequence 383748,
C 24	14	93.3	680	6	US-09-925-065A-596124	Sequence 596124,
C 25	14	93.3	686	6	US-09-925-065A-884458	Sequence 884458,
C 26	14	93.3	748	6	US-09-925-065A-947300	Sequence 947300,
C 27	14	93.3	753	6	US-09-925-065A-947492	Sequence 947492,
C 28	14	93.3	991	6	US-09-925-065A-2135	Sequence 2135, Ap
29	14	93.3	1045	8	US-10-750-185-44511	Sequence 44511, A
30	14	93.3	1045	8	US-10-750-185-44511	Sequence 44511, A
31	14	93.3	1072	8	US-10-750-185-35917	Sequence 35917, A
32	14	93.3	1072	8	US-10-750-185-35917	Sequence 35917, A
C 33	14	93.3	1522	8	US-10-750-185-43114	Sequence 43114, A
C 34	14	93.3	1522	8	US-10-750-185-43114	Sequence 43114, A
C 35	14	93.3	1564	8	US-10-750-185-60041	Sequence 60041, A
36	14	93.3	1564	8	US-10-750-185-60041	Sequence 60041, A
37	14	93.3	1685	8	US-10-750-185-64640	Sequence 64640, A
38	14	93.3	1685	8	US-10-750-185-64640	Sequence 64640, A
C 39	14	93.3	1692	8	US-10-873-528-235	Sequence 235, App
C 40	14	93.3	1692	8	US-10-873-528-235	Sequence 235, App
41	14	93.3	1805	8	US-10-750-185-39400	Sequence 39400, A
42	14	93.3	1805	8	US-10-750-185-39400	Sequence 39400, A
43	14	93.3	1937	8	US-10-750-185-59151	Sequence 59151, A
44	14	93.3	1937	8	US-10-750-185-59151	Sequence 59151, A
45	14	93.3	2280	8	US-10-750-185-35996	Sequence 35996, A
46	14	93.3	2280	8	US-10-750-185-35996	Sequence 35996, A
C 47	14	93.3	4378	12	US-11-136-527-2532	Sequence 2532, Ap
C 48	14	93.3	170837	12	US-11-121-086-97	Sequence 97, Appl
49	14	93.3	403278	12	US-10-995-561-13421	Sequence 13421, A
50	13.4	89.3	25	12	US-11-121-849-532232	Sequence 532232,
C 51	13.4	89.3	25	12	US-11-121-849-532233	Sequence 532233,
C 52	13.4	89.3	50	12	US-11-175-859-2668	Sequence 2668, Ap
C 53	13.4	89.3	50	12	US-11-175-859-2668	Sequence 2668, Ap
C 54	13.4	89.3	201	8	US-10-995-561-30308	Sequence 30308, A
C 55	13.4	89.3	201	8	US-10-995-561-61782	Sequence 61782, A
56	13.4	89.3	201	8	US-10-995-561-77745	Sequence 77745, A
57	13.4	89.3	411	6	US-09-925-065A-189701	Sequence 189701,
58	13.4	89.3	411	6	US-09-925-065A-189702	Sequence 189702,
59	13.4	89.3	445	6	US-09-925-065A-113294	Sequence 113294,
C 60	13.4	89.3	471	6	US-09-925-065A-146934	Sequence 146934,
C 61	13.4	89.3	474	6	US-09-925-065A-227031	Sequence 227031,
C 62	13.4	89.3	474	6	US-09-925-065A-409257	Sequence 409257,
C 63	13.4	89.3	474	6	US-09-925-065A-501244	Sequence 501244,
C 64	13.4	89.3	483	6	US-09-925-065A-470985	Sequence 470985,
65	13.4	89.3	493	6	US-09-925-065A-806810	Sequence 806810,
C 66	13.4	89.3	501	6	US-09-925-065A-535625	Sequence 535625,
C 67	13.4	89.3	503	6	US-09-925-065A-802293	Sequence 802293,
C 68	13.4	89.3	506	6	US-09-925-065A-802397	Sequence 802397,
69	13.4	89.3	506	6	US-09-925-065A-802535	Sequence 802535,
C 70	13.4	89.3	510	6	US-09-925-065A-284881	Sequence 284881,
C 71	13.4	89.3	510	6	US-09-925-065A-284882	Sequence 284882,
C 72	13.4	89.3	510	6	US-09-925-065A-802639	Sequence 802639,
C 73	13.4	89.3	511	6	US-09-925-065A-159739	Sequence 159739,
74	13.4	89.3	526	6	US-09-925-065A-771812	Sequence 771812,
75	13.4	89.3	530	6	US-09-925-065A-288917	Sequence 288917,
76	13.4	89.3	530	6	US-09-925-065A-288918	Sequence 288918,
77	13.4	89.3	530	6	US-09-925-065A-288919	Sequence 288919,
C 78	13.4	89.3	533	6	US-09-925-065A-629995	Sequence 629995,
C 79	13.4	89.3	537	6	US-09-925-065A-478261	Sequence 478261,
80	13.4	89.3	539	6	US-09-925-065A-579688	Sequence 579688,
C 81	13.4	89.3	539	6	US-09-925-065A-579689	Sequence 579689,
C 82	13.4	89.3	543	6	US-09-925-065A-233306	Sequence 233306,
C 83	13.4	89.3	544	6	US-09-925-065A-789644	Sequence 789644,
C 84	13.4	89.3	549	6	US-09-925-065A-268015	Sequence 268015,
C 85	13.4	89.3	549	6	US-09-925-065A-658604	Sequence 658604,
C 86	13.4	89.3	554	6	US-09-925-065A-627171	Sequence 627171,
C 87	13.4	89.3	557	6	US-09-925-065A-486215	Sequence 486215,
C 88	13.4	89.3	557	6	US-09-925-065A-563062	Sequence 563062,
C 89	13.4	89.3	561	6	US-09-925-065A-620462	Sequence 620462,
C 90	13.4	89.3	563	6	US-09-925-065A-86845	Sequence 86845, A
C 91	13.4	89.3	563	6	US-09-925-065A-379915	Sequence 379915,
C 92	13.4	89.3	563	6	US-09-925-065A-379916	Sequence 379916,
C 93	13.4	89.3	563	6	US-09-925-065A-695139	Sequence 695139,

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 02:41:34 ; Search time 1705.5 Seconds
(without alignments)
411.496 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 attcgaagagcaaa 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	129	3	BQ225964 AGENCOURT
2	15	100.0	179	1	AI071880 UI-R-C2-n
3	15	100.0	184	6	CF497100 MG1-0002T
4	15	100.0	203	1	AV371778 AV371778
5	15	100.0	310	7	CR465098 CR465098
6	15	100.0	317	1	AV559947 AV559947
7	15	100.0	363	9	BZ207934 CH230-279
8	15	100.0	367	3	BP629892 BP629892
9	15	100.0	382	3	BP638044 BP638044
10	15	100.0	381	1	AV566547 AV566547
11	15	100.0	402	3	BP661855 BP661855
12	15	100.0	408	8	CX714140 RFPQ1.18
13	15	100.0	416	3	BI298573 UI-R-CV2-
14	15	100.0	417	1	AA487404 aa487404
15	15	100.0	421	3	BP624041 BP624041
16	15	100.0	422	3	BP644816 BP644816
17	15	100.0	433	1	AI071117 UI-R-C2-m
18	15	100.0	435	3	BP786806 BP786806
19	15	100.0	437	3	CV504339 CV504339
20	15	100.0	439	10	CW762695 CW762695
21	15	100.0	445	5	BY059558 BY059558
22	15	100.0	446	7	CO242653 CO242653

23	15	100.0	453	3	BP029150 BP029150
24	15	100.0	482	1	AW869926 NXNV.120
25	15	100.0	499	1	AW226640 um57h10.y
26	15	100.0	505	2	BI071384 C056P77U
27	15	100.0	505	7	CN996996 Mdfw2043e
28	15	100.0	531	9	AZ556227 RPCI-23-1
29	15	100.0	554	1	AV769071 AV769071
30	15	100.0	561	7	CO250585 WS00811.B
31	15	100.0	563	10	CW513658 115 5 105
32	15	100.0	576	5	BX519784 BX519784
33	15	100.0	578	3	BJ559482 BJ559482
34	15	100.0	581	7	CK119279 218f21.pl
35	15	100.0	581	8	DR573692 WS00735.B
36	15	100.0	594	3	BI296694 UI-R-CV2-
37	15	100.0	594	7	CN997689 Mdfw2053m
38	15	100.0	594	9	AQ770337 HS 5333 A
39	15	100.0	611	8	DR090991 RT11.18
40	15	100.0	615	9	AQ725411 HS 5383 A
41	15	100.0	619	10	CW099364 104 466 1
42	15	100.0	628	7	CO244209 WS0037.B2
43	15	100.0	635	6	CB576979 AMGNNUC:U
44	15	100.0	637	9	BH361278 CH230-107
45	15	100.0	639	2	BB660768 BB660768
46	15	100.0	640	8	DR039899 BNS000032
47	15	100.0	645	9	CE127819 tigr-gss-
48	15	100.0	660	9	BH310733 CH230-129
49	15	100.0	663	1	AV782367 AV782367
50	15	100.0	673	10	AG066816 Pan trogl
51	15	100.0	676	1	AI812975 2C10 Pine
52	15	100.0	681	10	CE810128 tigr-gss-
53	15	100.0	691	11	CR000641 Reverse s
54	15	100.0	694	10	CW300712 104 784 1
55	15	100.0	697	1	AI919923 1453-Pine
56	15	100.0	703	9	CE060510 tigr-gss-
57	15	100.0	706	7	CN203794 Tor4031 G
58	15	100.0	708	10	CW300711 104 784 1
59	15	100.0	710	9	AZ593911 IM0405010
60	15	100.0	711	10	BX126468 Danio rer
61	15	100.0	714	5	BY720389 BY720389
62	15	100.0	727	9	BH929390 odi02h11.
63	15	100.0	737	6	CA125555 SCRL105
64	15	100.0	750	7	CV034980 RTNAC11.1
65	15	100.0	760	8	DN837917 SmoC-1 01
66	15	100.0	766	8	DR930330 EST112186
67	15	100.0	801	2	BG619554 602618946
68	15	100.0	822	9	BH703094 BOMNT43TF
69	15	100.0	828	1	AI920097 1627 Pine
70	15	100.0	834	8	DR579405 WS00751.C
71	15	100.0	840	6	CA492067 AGENCOURT
72	15	100.0	848	9	AQ751802 HS 5569 B
73	15	100.0	848	9	BZ117704 CH230-510
74	15	100.0	857	10	C2976585 178493 To
75	15	100.0	873	1	AJ816505 AJ816505
76	15	100.0	892	7	CV198033 CGF100395
77	15	100.0	906	2	CO238814 WS00722.B
78	15	100.0	919	7	BF138968 601784103
79	15	100.0	974	4	BM909843 AGENCOURT
80	15	100.0	1100	3	BM909843 AGENCOURT
81	15	100.0	1144	9	CC240920 CH261-10A
82	15	100.0	1517	2	BG390402 602416026
83	14	93.3	147	7	CK786054 UI-D-GC1-
84	14	93.3	187	3	BI437383 9C59H04.Y
85	14	93.3	218	1	AW036723 EST282721
86	14	93.3	221	3	BP877616 BP877616
87	14	93.3	233	9	BZ933187 CH240_88C
88	14	93.3	235	1	AW921146 EST352450
89	14	93.3	237	9	CC515846 CH240_361
90	14	93.3	237	1	AW838779 CM4-LT005
91	14	93.3	243	11	DE091018 Oryzias 1
92	14	93.3	245	1	AA140794 CK01012.5
93	14	93.3	245	3	BI574610 RH25903.5
94	14	93.3	262	1	AA405522 zw39all.1
95	14	93.3	265	2	BE433934 EST405012

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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 03:12:03 ; Search time 401.5 Seconds
(without alignments)
308.943 Million cell updates/sec

Title: US-10-804-470-2

Perfect score: 15

Sequence: 1 acttcaagagagcaa 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues.

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	8	US-10-804-470-2
2	15	100.0	25	7	US-10-719-956-571453
3	15	100.0	43	8	US-10-804-470-3
4	15	100.0	43	8	US-10-804-470-5
5	15	100.0	43	8	US-10-804-470-6
6	15	100.0	43	8	US-10-804-470-7
7	15	100.0	43	8	US-10-804-470-8
8	15	100.0	1820	7	US-10-437-963-97628
9	15	100.0	2796	7	US-10-437-963-97626
10	15	100.0	3335	7	US-10-437-963-97629
11	14	93.3	25	7	US-10-719-956-93565
12	14	93.3	41	3	US-09-765-272-389
13	14	93.3	41	10	US-11-106-649-389
14	14	93.3	373	8	US-10-357-930-47159
15	14	93.3	378	3	US-09-925-065A-95610
16	14	93.3	429	4	US-09-925-065A-95610
17	14	93.3	434	3	US-09-814-353-4767
18	14	93.3	434	3	US-09-814-353-11064
19	14	93.3	503	8	US-10-357-930-46982
20	14	93.3	520	4	US-09-925-065A-404803
21	14	93.3	543	4	US-09-925-065A-340164
22	14	93.3	559	4	US-09-925-065A-156850
23	14	93.3	584	9	US-10-972-079-71790

C 24	14	93.3	585	3	US-09-814-353-17448	Sequence 17448, A
C 25	14	93.3	587	4	US-09-925-065A-457748	Sequence 457748, A
C 26	14	93.3	594	5	US-10-027-632-218198	Sequence 218198, A
C 27	14	93.3	594	6	US-10-027-632-218198	Sequence 218198, A
C 28	14	93.3	603	8	US-10-425-115-106630	Sequence 106630, A
C 29	14	93.3	609	4	US-09-925-065A-835726	Sequence 835726, A
C 30	14	93.3	610	8	US-10-425-115-44512	Sequence 44512, A
C 31	14	93.3	611	4	US-09-925-065A-383746	Sequence 383746, A
C 32	14	93.3	611	4	US-09-925-065A-383747	Sequence 383747, A
C 33	14	93.3	611	4	US-09-925-065A-383748	Sequence 383748, A
C 34	14	93.3	680	4	US-09-925-065A-596124	Sequence 596124, A
C 35	14	93.3	686	4	US-09-925-065A-884458	Sequence 884458, A
C 36	14	93.3	748	4	US-09-925-065A-947100	Sequence 947100, A
C 37	14	93.3	753	4	US-09-925-065A-947492	Sequence 947492, A
C 38	14	93.3	784	3	US-09-765-272-163	Sequence 163, App
C 39	14	93.3	784	10	US-11-106-649-163	Sequence 163, App
C 40	14	93.3	856	8	US-10-425-115-180559	Sequence 180559, A
C 41	14	93.3	881	8	US-10-739-930-5348	Sequence 5348, App
C 42	14	93.3	991	4	US-09-925-065A-2135	Sequence 2135, App
C 43	14	93.3	1116	7	US-10-724-972A-280	Sequence 280, App
C 44	14	93.3	1134	9	US-10-617-320-1717	Sequence 1717, App
C 45	14	93.3	1363	8	US-10-425-115-90531	Sequence 90531, A
C 46	14	93.3	1410	3	US-09-828-302-10	Sequence 10, Appl
C 47	14	93.3	1410	7	US-10-764-259-10	Sequence 10, Appl
C 48	14	93.3	1689	8	US-10-472-928-1231	Sequence 1231, App
C 49	14	93.3	1692	3	US-09-769-787-235	Sequence 235, App
C 50	14	93.3	1692	3	US-09-769-787-236	Sequence 236, App
C 51	14	93.3	1955	7	US-10-424-599-56749	Sequence 56749, A
C 52	14	93.3	2133	7	US-10-437-963-80549	Sequence 80549, A
C 53	14	93.3	2467	7	US-10-424-599-4901	Sequence 4901, App
C 54	14	93.3	2947	7	US-10-437-963-74398	Sequence 74398, A
C 55	14	93.3	2977	8	US-10-425-115-90533	Sequence 90533, A
C 56	14	93.3	3068	8	US-10-739-930-5312	Sequence 5312, App
C 57	14	93.3	3135	3	US-09-800-396-1	Sequence 1, Appli
C 58	14	93.3	3135	3	US-09-878-672-1	Sequence 1, Appli
C 59	14	93.3	3135	3	US-09-878-672-1	Sequence 1, Appli
C 60	14	93.3	3164	5	US-10-027-632-112475	Sequence 112475, A
C 61	14	93.3	3164	5	US-10-027-632-112476	Sequence 112476, A
C 62	14	93.3	3164	5	US-10-027-632-112477	Sequence 112477, A
C 63	14	93.3	3164	5	US-10-027-632-112477	Sequence 112477, A
C 64	14	93.3	3164	6	US-10-027-632-112475	Sequence 112475, A
C 65	14	93.3	3164	6	US-10-027-632-112475	Sequence 112475, A
C 66	14	93.3	3164	6	US-10-027-632-112477	Sequence 112477, A
C 67	14	93.3	4008	10	US-11-097-143-27508	Sequence 27508, A
C 68	14	93.3	4085	9	US-10-756-149-2536	Sequence 2536, App
C 69	14	93.3	4085	9	US-10-988-192A-1	Sequence 1, Appli
C 70	14	93.3	4174	6	US-10-101-510-408	Sequence 408, App
C 71	14	93.3	4345	9	US-10-450-763-22054	Sequence 22054, A
C 72	14	93.3	4361	7	US-10-152-319A-1729	Sequence 1729, App
C 73	14	93.3	5217	10	US-11-097-143-29512	Sequence 29512, A
C 74	14	93.3	5554	6	US-10-101-510-786	Sequence 786, App
C 75	14	93.3	6317	9	US-10-826-448-3	Sequence 3, Appli
C 76	14	93.3	10785	3	US-09-764-878-324	Sequence 324, App
C 77	14	93.3	10785	3	US-10-079-854-324	Sequence 324, App
C 78	14	93.3	13315	3	US-09-764-878-328	Sequence 328, App
C 79	14	93.3	13315	5	US-09-764-878-328	Sequence 328, App
C 80	14	93.3	13926	2	US-08-961-527-5	Sequence 5, Appli
C 81	14	93.3	13926	7	US-10-158-844-5	Sequence 5, Appli
C 82	14	93.3	20261	3	US-09-764-878-325	Sequence 325, App
C 83	14	93.3	20261	5	US-10-079-854-325	Sequence 325, App
C 84	14	93.3	25464	6	US-10-374-228-4	Sequence 325, App
C 85	14	93.3	150351	7	US-10-322-281-453	Sequence 453, App
C 86	14	93.3	185548	5	US-10-175-523-62	Sequence 62, Appl
C 87	14	93.3	185548	10	US-11-099-266-62	Sequence 1095, App
C 88	14	93.3	358246	6	US-10-292-798-1095	Sequence 1095, App
C 89	14	93.3	401035	7	US-10-741-601-5729	Sequence 5729, App
C 90	14	93.3	216298	8	US-10-472-928-4979	Sequence 4979, App
C 91	13.4	89.3	24	9	US-10-491-449A-3	Sequence 3, Appli
C 92	13.4	89.3	25	7	US-10-719-956-571452	Sequence 571452, A
C 93	13.4	89.3	25	8	US-10-719-900-39314	Sequence 39314, A
C 94	13.4	89.3	25	8	US-10-719-900-61964	Sequence 61964, A
C 95	13.4	89.3	25	9	US-10-956-157-310036	Sequence 310036, A
C 96	13.4	89.3	30	6	US-10-281-845A-7	Sequence 7, Appli